OM protein - protein search, using sw model

                    GenCore version 5.1.7
        Copyright (c) 1993 - 2006   Bioceleration Ltd.

Run on: March 29, 2006, 03:02:19 ; Search time 255 Seconds
                                       (without alignments)
                            3176.261 Million cell updates/sec

Title: US-09-824-575A-2
Perfect score: 5981
Sequence: 1 MSRATSVGDQLEAPARTIYL.........VSQBEVIRAYDTTKKSRKK 1148

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt 05.80:*
             1: uniprot_sprot:*
             2: uniprot_trembl:*

'Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

                            SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	5954	99.5	1148	1	AT8A2_HUMAN	Q9nt12 homo sapien
2	5951	99.5	1188	1	Q6ZSP3_HUMAN	Q6zsp3 homo sapien
3	5661	94.6	1148	1	AT8A2_MOUSE	P98200 mus musculu
4	4923.5	82.3	968	2	Q6ZU25_HUMAN	Q6zu25 homo sapien
5	4166.5	69.7	1164	2	Q8BR88_MOUSE	Q8br88 mus musculu
6	4166.5	69.7	1195	2	Q5DTG0_MOUSE	Q5dtg0 mus musculu
7	4157.5	69.5	1164	1	AT8A1_HUMAN	Q9y2q0 homo sapien
8	4113	69.1	1149	1	AT8A1_MOUSE	P70704 mus musculu
9	4113	68.8	1177	2	Q59EX4_HUMAN	Q59ex4 homo sapien
10	4107	68.7	1149	1	AT8A1_BOVIN	Q29449 bos taurus
11	4003	66.9	1247	2	Q4RTG6_TETNG	Q4rtg6 tetraodon n
12	3372	56.4	947	2	Q4S557_TETNG	Q4s557 tetraodon n
13	3265	54.6	1150	2	Q8T014_DROME	Q8t014 drosophila
14	3249.5	54.3	1235	2	Q9V6P5_DROME	Q9v6p5 drosophila
15	3249.5	54.3	1360	2	Q8ML69_DROME	Q8ml69 drosophila
16	3212	53.7	1076	2	Q7PMY3_ANOGA	Q7pmy3 anopheles g
17	3187.5	53.3	1216	2	Q6AWM7_DROME	Q6awm7 drosophila
18	2928.5	49.0	806	2	Q52KQ7_MOUSE	Q52kq7 mus musculu
19	2711.5	45.3	1357	2	Q4X1T4_ASPFU	Q4x1t4 aspergillus
20	2695	45.1	1348	2	Q5B018_EMENI	Q5b018 aspergillus
21	2655	44.4	1333	2	Q6C314_YARLI	Q6c314 yarrowia li
22	2642	44.2	1384	2	Q4P669_USTMA	Q4p669 ustilago ma
23	2640	44.1	1258	2	O94296_SCHPO	O94296 schizosacch
24	2636	44.1	1363	2	Q4I7R5_GIBZE	Q4i7r5 gibberella
25	2633.5	44.0	1305	2	Q9P424_AJECA	Q9p424 ajellomyces
26	2610.5	43.6	1133	2	Q61F70_CAEBR	Q61f70 caenorhabdi
27	2600	43.5	1360	2	Q7RZL3_NEUCR	Q7rzl3 neurospora
28	2582	43.2	1343	2	Q6CY12_KLULA	Q6cy12 kluyveromyc
29	2569.5	43.0	1139	2	Q9U280_CAEEL	Q9u280 caenorhabdi
30	2549.5	42.6	1320	2	Q5ADR3_CANAL	Q5adr3 candida alb
31	2535.5	42.2	1328	2	Q6FT10_CANGA	Q6ft10 candida gla
32	2513	42.0	1355	1	ATC3_YEAST	P39524 saccharomyc
33	2506.5	41.9	1089	2	Q7JK70_CAEBL	Q7jk70 caenorhabdi
34	2498	41.8	1326	2	Q5KP96_CRYNE	Q5kp96 cryptococcu
35	2487	41.6	1328	2	Q55ZY9_CRYNE	Q55zy9 cryptococcu
36	2425.5	40.6	1313	2	Q55E61_DICDI	Q55e61 dictyosteli
37	2362.5	39.5	1311	2	Q759C7_ASHGO	Q759c7 ashbya goss
38	2241.5	37.5	1209	1	AT8B2_HUMAN	P98198 homo sapien
39	2239.5	37.4	1223	2	Q7Z486_HUMAN	Q7z486 homo sapien
40	2235.5	37.4	1201	2	Q4RTU6_TETNG	Q4rtu6 tetraodon n
41	2231.5	37.3	1250	2	Q5BL50_XENTR	Q5bl50 xenopus tro
42	2225	37.2	1192	1	AT8B4_HUMAN	Q8tf62 homo sapien
43	2223	37.2	1251	1	AT8B1_HUMAN	O43520 homo sapien
44	2221	37.1	1213	2	ALA3_ARATH	Q9xie6 arabidopsis
45	2209	36.9	1251	2	Q6R964_MOUSE	Q6r964 mus musculu

                            ALIGNMENTS

RESULT 1
AT8A2_HUMAN
ID   AT8A2_HUMAN   STANDARD;   PRT; 1148 AA.
AC   Q9NT12; Q9H527; Q9NPU6; Q9NYM3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Potential phospholipid-transporting ATPase IB   (EC 3.6.3.1) (ATPase
DE   class I type 8A member 2) (ML-1).
GN   Name=ATP8A2; Synonyms=ATPIB;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 2).
RA   Sun X.L., Milo G.E., Li D.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15057823; DOI=10.1038/nature02379;
RA   Dunham A., Matthews L.H., Burton J., Ashurst J.L., Howe K.L.,
RA   Ashcroft K.J., Beare D.M., Burford D.C., Hunt S.E.,
RA   Griffiths-Jones S., Jones M.C., Keenan S.J., Oliver K., Scott C.E.,
RA   Ainscough R., Almeida J.P., Ambrose K.D., Andrews D.T.,
RA   Ashwell R.I.S., Babbage A.K., Bagguley C.L., Bailey J., Bannerjee R.,
RA   Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,
RA   Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M.B., Clark S.Y., Clarke G., Clee C.M.,
RA   Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,
RA   Deloukas P., Dhami P., Dunham I., Dunn M., Earthrowl M.E.,
RA   Ellington A.G., Faulkner L., Frankish A.G., Frankland J., French L.,
RA   Garner P., Garnett J., Gilbert J.G.R., Gilson C.J., Ghori J.,
RA   Grafham D.V., Gribble S.M., Griffiths C., Hall R.E., Hammond S.,
RA   Harley J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,
RA   Hunt P.J., Hunt A.R., Johnson C., Johnson D., Kay M., Kimberley A.M.,
RA   King A., Laird G.K., Langford C.J., Lawlor S., Leongamornlert D.A.,
RA   Lloyd D.M., Lloyd C., Loveland J.E., Lovell J., Martin S.,
RA   Mashreghi-Mohammadi M., McLaren S.J., McMurray A., Milne S.,
RA   Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,
RA   Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,
RA   Sehra H.K., Shownkeen R., Skuce C.D., Smith M., Steward C.A.,
RA   Sycamore N., Tester J., Thomas D.W., Tracey A., Tromans A., Tubby B.,
RA   Wall M., Wallis J.M., West A.P., Whitehead S.L., Willey D.L.,
RA   Wilming L., Wray P.W., Wright M.W., Young L., Coulson A., Durbin R.,
RA   Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.;
RT   "The DNA sequence and analysis of human chromosome 13.";
RL   Nature 428:522-528(2004).
RN   [3]
RP   PARTIAL NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20017962; PubMed=10551800;
RA   Sun X.L., Li D., Fang J., Noyes I., Casto B., Theil K., Shuler C.,
RA   Milo G.E.;

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              GenCore version 5.1.7
       Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:       March 29, 2006, 03:11:59 ; Search time 26 Seconds
                                          (without alignments)
                                          1302.290 Million cell updates/sec

Title:        US-09-824-575A-2
Perfect score: 5981
Sequence:     1 MSRATSVGDQLEAPARTIYL..........VSQEVIRAYDTTKKKSRKK 1148

Scoring.table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:     174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters:        174695

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA_New:*
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             2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
             3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
             4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
             5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
             6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
             7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
             8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2226.5	37.2	1190	7	US-11-043-889-20	Sequence 20, Appl
2	2223	37.2	1251	7	US-11-043-889-22	Sequence 22, Appl
3	2103	35.2	1216	7	US-11-096-568A-28970	Sequence 28970, A
4	2079	34.8	1218	7	US-11-096-568A-31175	Sequence 31175, A
5	2073	34.7	1166	7	US-11-096-568A-30808	Sequence 30808, A
6	2073	34.7	1174	7	US-11-096-568A-30807	Sequence 30807, A
7	2066.5	34.6	1167	7	US-11-096-568A-28971	Sequence 28971, A
8	2061.5	34.5	1181	7	US-11-096-568A-27847	Sequence 27847, A
9	2061.5	34.5	1189	7	US-11-096-568A-27846	Sequence 27846, A
10	2042.5	34.1	1169	7	US-11-096-568A-31176	Sequence 31176, A
11	2032.5	34.0	1184	7	US-11-096-568A-29280	Sequence 29280, A
12	1941	32.5	1057	7	US-11-096-568A-30809	Sequence 30809, A
13	1939	32.4	1108	7	US-11-096-568A-28972	Sequence 28972, A
14	1929.5	32.3	1072	7	US-11-096-568A-27848	Sequence 27848, A
15	1915	32.0	1110	7	US-11-096-568A-31177	Sequence 31177, A
16	1897.5	31.7	1063	7	US-11-096-568A-29281	Sequence 29281, A
17	1797	30.0	1134	7	US-11-043-889-34	Sequence 34, Appl
18	1759	29.4	1508	7	US-11-043-889-47	Sequence 47, Appl
19	1753	29.3	1187	7	US-11-043-889-46	Sequence 46, Appl
20	1733	29.0	989	7	US-11-096-568A-29282	Sequence 29282, A
21	1680	28.1	1588	7	US-11-043-889-37	Sequence 37, Appl
22	1268	21.2	1194	7	US-11-000-463-249	Sequence 249, App
23	1265	21.2	1070	7	US-11-000-463-721	Sequence 721, App
24	1221	20.4	877	6	US-10-821-234-960	Sequence 960, App
25	1047.5	17.5	756	6	US-10-330-773-731	Sequence 731, App
26	1042	17.4	736	7	US-11-072-512-3774	Sequence 3774, Ap
27	1029.5	17.2	912	6	US-10-501-035-372	Sequence 372, App
28	751.5	12.6	529	7	US-11-072-512-2137	Sequence 2137, Ap
29	739.5	12.4	501	6	US-10-537-002-61	Sequence 61, Appl
30	595.5	10.0	376	7	US-11-096-568A-7703	Sequence 7703, Ap
31	556	9.3	255	6	US-10-330-773-734	Sequence 734, App
32	552.5	9.2	340	7	US-11-096-568A-7704	Sequence 7704, Ap
33	550.5	9.2	337	7	US-11-096-568A-7705	Sequence 7705, Ap
34	389.5	6.5	890	6	US-10-510-386-26	Sequence 26, Appl
35	375.5	6.3	1015	7	US-10-957-569-51	Sequence 51, Appl
36	375.5	6.3	1015	7	US-10-097-589-50	Sequence 50, Appl
37	356.5	6.0	1220	6	US-10-501-035-260	Sequence 260, App
38	327	5.5	919	7	US-11-074-176-284	Sequence 284, App
39	315.5	5.3	892	7	US-11-082-389-396	Sequence 396, App
40	307	5.1	997	6	US-10-501-035-238	Sequence 238, App
41	296	4.9	388	7	US-11-072-512-3764	Sequence 3764, Ap
42	293.5	4.9	1023	6	US-10-821-234-1377	Sequence 1377, Ap
43	198	3.3	946	7	US-11-010-239-42	Sequence 42, Appl
44	166	2.8	775	6	US-10-467-657-4032	Sequence 4032, Ap
45	142.5	2.4	1001	6	US-10-467-962B-81	Sequence 81, Appl

ALIGNMENTS

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RESULT 1
US-11-043-889-20
; Sequence 20, Application US/11043889
; Publication No. US20060008819A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT: Gluckman, Maria Alexandra
;  APPLICANT: Meyers, Rachel E.
;  TITLE OF INVENTION: NOVEL 38594, 57312, 53659, 57250, 63760, 49938, 32146,
;  TITLE OF INVENTION: 57259, 67118, 67067, 62092, FBH58295FL, 57255,
;  TITLE OF INVENTION: AND 57255alt MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MPI02-095DV1OMNIM
;  CURRENT APPLICATION NUMBER: US/11/043,889
;  CURRENT FILING DATE: 2005-01-26
;  PRIOR APPLICATION NUMBER: US 10/154,419
;  PRIOR FILING DATE: 2002-05-22
;  PRIOR APPLICATION NUMBER: US 09/858194
;  PRIOR FILING DATE: 2001-05-14
;  PRIOR APPLICATION NUMBER: US 60/204211
;  PRIOR FILING DATE: 2000-05-12
;  PRIOR APPLICATION NUMBER: US 09/895811
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/215376
;  PRIOR FILING DATE: 2000-06-29
;  PRIOR APPLICATION NUMBER: US 09/919781
;  PRIOR FILING DATE: 2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/221769
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/957664
;  PRIOR FILING DATE: 2001-09-19
;  PRIOR APPLICATION NUMBER: US 60/233790
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: US 09/964295
;  PRIOR FILING DATE: 2001-09-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: FastSEQ Version 4.0
;  SEQ ID NO 20
;  LENGTH: 1190
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-11-043-889-20

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  Matches  469;  Conservative  210;  Mismatches  380;  Indels   89;  Gaps   18;

Qy         27 KFRDNRISTAKYSVLTFLPRFLYEQIRRAANAFPLFIALLQQIPDVSPTGRYTTLVPLII 86
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             GenCore version 5.1.7
        Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:   March 29, 2006, 03:10:59 ; Search time 177 Seconds
                               (without alignments)
                      2709.989 Million cell updates/sec

Title:       US-09-824-575A-2
Perfect score: 5981
Sequence:   1 MSRATSVGDQLEAPARTIYL.........VSQEEVIRAYDTTKKKSRKK 1148

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:   1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:   1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Published Applications AA Main:*
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    4: /cgn2_6/ptcdata/1/pubpaa/US10A_PUBCOMB.pep:*
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    6: /cgn2_6/ptcdata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match %	Match Length	DB	ID	Description
1	5954	99.5	1176	4	US-10-041-395-2	Sequence 2, Appli
2	5661	94.6	1148	5	US-10-732-923-22564	Sequence 22564, A
3	4944	82.7	994	5	US-10-732-923-22746	Sequence 22746, A
4	4363	72.9	883	4	US-10-041-395-5	Sequence 5, Appli
5	4166.5	69.7	1164	5	US-10-732-923-22563	Sequence 22563, A
6	4157.5	69.5	1164	5	US-10-732-923-22727	Sequence 22727, A
7	4153.5	69.4	1161	4	US-10-170-102-4	Sequence 4, Appli
8	4153.5	69.4	1161	5	US-10-732-923-22728	Sequence 22728, A
9	4133.5	69.1	1193	4	US-10-467-685-2	Sequence 2, Appli
10	4133	69.1	1149	5	US-10-732-923-22562	Sequence 22562, A
11	4119	68.9	790	5	US-10-732-923-22731	Sequence 22731, A
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13	3793	63.4	729	5	US-10-732-923-22733	Sequence 22733, A
14	3302.5	55.2	1142	5	US-10-732-923-22578	Sequence 22578, A
15	3265	54.6	1150	5	US-10-732-923-22717	Sequence 22717, A
16	3249.5	54.3	1235	5	US-10-732-923-22719	Sequence 22719, A
17	3249.5	54.3	1360	5	US-10-732-923-22718	Sequence 22718, A
18	3220.5	53.8	1297	6	US-11-097-143-25221	Sequence 25221, A
19	3171	53.0	613	5	US-10-732-923-22739	Sequence 22739, A
20	2865.5	47.9	1352	5	US-10-732-923-22570	Sequence 22570, A
21	2640	44.1	1104	4	US-10-369-493-22548	Sequence 22548, A
22	2640	44.1	1258	4	US-10-310-154-703	Sequence 703, App
23	2640	44.1	1258	5	US-10-732-923-621	Sequence 621, App
24	2640	44.1	1258	5	US-10-732-923-22696	Sequence 22696, A
25	2633.5	44.0	1305	5	US-10-732-923-22697	Sequence 22697, A
26	2600	43.5	1360	5	US-10-369-493-3557	Sequence 3557, Ap
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29	2513	42.0	1355	4	US-10-310-154-702	Sequence 702, App
30	2513	42.0	1355	4	US-10-369-493-1388	Sequence 1388, Ap
31	2513	42.0	1355	5	US-10-732-923-620	Sequence 620, App
32	2513	42.0	1355	5	US-10-732-923-22760	Sequence 22760, A
33	2310	38.6	1035	4	US-10-369-493-12862	Sequence 12862, A
34	2239.5	37.4	1190	4	US-10-332-447-4	Sequence 4, Appli
35	2239.5	37.4	1566	5	US-10-499-352A-523	Sequence 523, App
36	2231.5	37.3	1190	5	US-10-490-556-2	Sequence 2, Appli
37	2226.5	37.2	1190	4	US-09-964-295-2	Sequence 2, Appli
38	2226.5	37.2	1190	4	US-10-154-419-20	Sequence 20, Appli
39	2223	37.2	1251	3	US-09-964-295-4	Sequence 4, Appli
40	2223	37.2	1251	4	US-10-154-419-22	Sequence 22, Appl
41	2223	37.2	1251	4	US-10-295-027-1210	Sequence 1210, Ap
42	2223	37.2	1251	4	US-10-188-832-70	Sequence 70, Appl
43	2223	37.2	1251	5	US-10-732-923-22729	Sequence 22729, A
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45	2221	37.1	1213	5	US-10-732-923-22589	Sequence 22589, A

ALIGNMENTS

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; Sequence 2, Application US/1041395
; Publication No. US20020119523A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J
; TITLE OF INVENTION: 67073, A Human Phospholipid Transporter
; TITLE OF INVENTION:  Family Member and Uses Therefor
; FILE REFERENCE: MPI2001-015P2R(M)
; CURRENT APPLICATION NUMBER: US/10/041,395
; CURRENT FILING DATE:  2002-01-08
; PRIOR APPLICATION NUMBER: 60/262,216
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/289,358
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1176
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-041-395-2

Query Match             99.5%;  Score 5954;  DB 4;  Length 1176;
Best Local Similarity   99.7%;  Pred. No. 0;
Matches 1144;  Conservative 2;  Mismatches 2;  Indels 0;  Gaps 0;

Qy      1 MSRATSVGDQLEAPARTIYLNQPHLNKFRDNRISTAKYSVLTFLPRFLYEQIRRAANAFF 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     29 MSRATSVGDQLEAPARTIYLNQPHLNKFRDNQISTAKYSVLTFLPRFLYEQIRRAANAFF 88

Qy     61 LFIALLQQIPDVSPTGRYTTLVPLIIILTIAGIKGIVEDFKRHKADNAVNKKKTIVLRNG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     89 LFIALLQQIPDVSPTGRYTTLVPLIIILTIAGIKBIVEDFKRHKADNAVNKKKTIVLRNG 148

Qy    121 MWHTIMWKEVAVGDIVKVVNGQYLPADVVLLSSSEPQAMCYVETANLDGETNLKIRQGLS 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    149 MWHTIMWKEVAVGDIVKVVNGQYLPADVVLLSSSEPQAMCYVETANLDGETNLKIRQGLS 208

Qy    181 HTADMQTREVLMKLSGTIBCEGPNRHLYDFTGNLNLDGKSLVALGPDQILLRGTQLRNTQ 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    209 HTADMQTREVLMKLSGTIBCEGPNRHLYDFTGNLNLDGKSLVALGPDQILLRGTQLRNTQ 268

Qy    241 WVFGIVVYTGHDTKLMQNSTKAPLKRSNVEKVTNVQILLVLFGILLVMALVSSAGALYWNR 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    269 WVFGIVVYTGHDTKLMQNSTKAPLKRSNVEKVTNVQILLVLFGILLVMALVSSAGALYWNR 328

Qy    301 SHGSKNWYIKWGDTTSDNFGYNLLTFIILYNNLIPISLLVTLBVVKYTQALPINWDTDMY 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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                    GenCore version 5.1.7
        Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:    March 29, 2006, 03:10:04 ; Search time 50 Seconds
                                      (without alignments)
                                      1898.234 Million cell updates/sec

Title:          US-09-824-575A-2
Perfect score:  5981
Sequence:       1 MSRATSVGDQLEAPARTIYL.........VSQEEVIRAYDTTKKKSRKK 1148

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:       572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:    572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database ::  Issued Patents AA:*
     1: /cgn2_6/ptcdata/1/iaa/5_COMB.pep:*
     2: /cgn2_6/ptcdata/1/iaa/6_COMB.pep:*
     3: /cgn2_6/ptcdata/1/iaa/H_COMB.pep:*
     4: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
     5: /cgn2_6/ptcdata/1/iaa/RE_COMB.pep:*
     6: /cgn2_6/ptcdata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3191	53.4	615	2	US-09-949-016-9602	Sequence 9602, Ap
2	2223	37.2	1251	2	US-09-949-016-7784	Sequence 7784, Ap
3	1802	30.1	1177	2	US-09-795-927-2	Sequence 2, Appl
4	1778	29.7	1426	2	US-09-710-092-14	Sequence 14, Appl
5	1778	29.7	1426	2	US-10-231-354-14	Sequence 14, Appl
6	1745.5	29.2	1270	2	US-09-710-092-10	Sequence 10, Appl
7	1745.5	29.2	1270	2	US-10-231-354-10	Sequence 10, Appl
8	1729	29.2	1395	2	US-09-949-016-7109	Sequence 7109, Ap
9	1393	23.3	822	2	US-09-248-796A-20787	Sequence 20787, A
10	1326.5	22.2	1056	2	US-09-710-092-6	Sequence 6, Appli
11	1326.5	22.2	1056	2	US-10-231-354-6	Sequence 6, Appli
12	1181.5	19.8	972	2	US-09-710-092-2	Sequence 2, Appli
13	1181.5	19.8	972	2	US-10-231-354-2	Sequence 2, Appli
14	1042	17.4	736	2	US-10-104-047-3774	Sequence 3774, Ap
15	947.5	15.8	818	2	US-09-248-796A-20792	Sequence 20792, A
16	869.5	14.5	324	2	US-09-248-796A-20753	Sequence 20753, A
17	852.5	14.3	578	2	US-09-710-092-16	Sequence 16, Appl
18	852.5	14.3	578	2	US-10-231-354-16	Sequence 16, Appl
19	820	13.7	422	2	US-09-710-092-12	Sequence 12, Appl
20	820	13.7	422	2	US-10-231-354-12	Sequence 12, Appl
21	814	13.6	622	2	US-09-270-767-44449	Sequence 44449, A
22	805.5	13.5	815	2	US-09-248-796A-20788	Sequence 20788, A
23	751.5	12.6	529	2	US-10-104-047-2137	Sequence 2137, Ap
24	637.5	10.7	570	2	US-09-248-796A-18607	Sequence 18607, A
25	539.5	9.0	451	2	US-09-248-796A-20754	Sequence 20754, A
26	534	8.9	374	2	US-09-795-927-4	Sequence 4, Appli
27	503.5	8.4	255	2	US-09-270-767-33855	Sequence 33855, A
28	503.5	8.4	255	2	US-09-270-767-49072	Sequence 49072, A
29	425	7.1	225	2	US-09-248-796A-20752	Sequence 20752, A
30	422	7.1	331	2	US-09-248-796A-20795	Sequence 20795, A
31	408	6.8	1198	2	US-09-949-016-6109	Sequence 6109, Ap
32	406.5	6.8	185	2	US-09-248-796A-20789	Sequence 20789, A
33	401	6.7	208	2	US-09-710-092-8	Sequence 8, Appli
34	401	6.7	208	2	US-10-231-354-8	Sequence 8, Appli
35	391.5	6.5	1179	2	US-09-949-016-10545	Sequence 10545, A
36	390.5	6.5	239	2	US-09-270-767-59887	Sequence 59887, A
37	358.5	6.0	1225	2	US-09-949-016-9468	Sequence 9468, Ap
38	354	5.9	898	2	US-09-583-110-3327	Sequence 3327, Ap
39	354	5.9	916	2	US-09-107-433-2987	Sequence 2987, Ap
40	328	5.5	719	2	US-09-107-532A-5992	Sequence 5992, Ap
41	326	5.5	1141	2	US-09-949-016-9459	Sequence 9459, Ap
42	324	5.4	829	2	US-09-270-767-46176	Sequence 46176, A
43	305.5	5.1	690	2	US-09-949-016-8803	Sequence 8803, Ap
44	303	5.1	84	2	US-09-513-999C-6727	Sequence 6727, Ap
45	301.5	5.0	1031	2	US-09-949-016-7849	Sequence 7849, Ap

ALIGNMENTS

```
RESULT 1
US-09-949-016-9602

Sequence 9602, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9602
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9602

Query Match        53.4%;  Score 3191;  DB 2;  Length 615;
Best Local Similarity  99.7%;  Pred. No. 0;
Matches  613;  Conservative  0;  Mismatches  0;  Indels  2;  Gaps  0;

Qy    534  KRMSVIVRTPSGRLRLYCKGADNVIFERLSKDSKYMEETLCHLEYFATEGLRTLCVAYAD 593
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  KRMSVIVRTPSGRLRLYCKGADNVIFERLSKDSKYMEETLCHLEYFATEGLRTLCVAYAD 60

Qy    594  LSENEYEEWLKVYQEASTILKDRAQRLEECYEIIEKNLLLLGATAIEDRLQAGVPETIAT 653
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  LSENEYEEWLKVYQEASTILKDRAQRLEECYEIIEKNLLLLGATAIEDRLQAGVPETIAT 120

Qy    654  LLKABIKIWVLTGDKQETAINIGYSCRLVSQNMALILLKEDSLDATRAAITQHCTDLGNL 713
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  LLKABIKIWVLTGDKQETAINIGYSCRLVSQNMALILLKEDSLDATRAAITQHCTDLGNL 180

Qy    714  LGKENDVALIIDGHTLKYALSFEVRRSFLDLALSCKAVICCRVSPLQKSBIVDVVKKRVK 773
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  LGKENDVALIIDGHTLKYALSFEVRRSFLDLALSCKAVICCRVSPLQKSBIVDVVKKRVK 240

Qy    774  AITLAIGDGANDVGMIQTAHVGVGISGNEGMQATNNSDYAIAQFSYLEKLLVHGAWSYN 833
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  AITLAIGDGANDVGMIQTAHVGVGISGNEGMQATNNSDYAIAQFSYLEKLLVHGAWSYN 300

Qy    834  RVTKCILYCFYKNVVLYIIELWPAPVNGFSGQILFERWCIGLYNVIFTALPPFTLGIFER 893
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                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:      March 29, 2006, 03:05:44 ; Search time 50 Seconds
                                          (without alignments)
                                  2209.137 Million cell updates/sec

Title:       US-09-824-575A-2
Perfect score: 5981
Sequence:    1 MSRATSVGDQLEAPARTIYL.........VSQEEVIRAYDTTKKKSRKK 1148

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:    283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:    283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
             1: pir1:*
             2: pir2:*
             3: pir3:*
             4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                           SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	4133	69.1	1149	2	T30869	probable adenosine
2	4107	68.7	1149	2	T18515	adenosinetriphosph
3	3793	63.4	729	2	T46328	probable adenosine
4	2640	44.1	1258	2	T40737	probable calcium-t
5	2513	42.0	1355	2	S51995	probable ATPase (B
6	2216.5	37.1	1123	2	C96622	probable ATPase F2
7	2090	34.9	1228	2	G96751	hypothetical prote
8	2085.5	34.9	1244	2	C96584	hypothetical prote
9	2032.5	34.0	1184	2	D86387	probable protein P
10	2032	34.0	1200	2	F96711	hypothetical prote
11	1991	33.3	1203	2	F86266	probable phospholi
12	1842	30.8	1571	2	S50669	hypothetical prote
13	1812.5	30.0	1402	2	S62557	probable calcium-t
14	1795	30.0	1612	2	S51243	probable ATPase (B
15	1701	28.4	1367	2	T38820	probable calcium-t
16	1582.5	26.5	1656	2	S54520	probable membrane
17	1574	26.3	1353	2	T26301	hypothetical prote
18	1524	25.5	632	2	T27057	adenosinetriphosph
19	1444	24.1	1553	2	S67483	protein T24H7.5b [
20	1426.5	23.9	1454	2	C88175	protein T24H7.5a [
21	1424.5	23.8	1212	2	D88175	probable calcium-t
22	1229	20.5	1033	2	T39030	probable membrane
23	1194.5	20.0	1151	2	S48431	probable E1-E2 ATP
24	1192	19.9	1020	2	T42229	hypothetical prote
25	1167.5	19.5	1059	2	T21891	hypothetical prote
26	1146	19.2	221	2	T51867	hypothetical prote
27	1119	18.7	1864	2	T18485	hypothetical prote
28	985	16.5	626	2	D88601	protein Y49E10.11
29	938	15.7	1156	2	T14899	aminophospholipid
30	872.5	14.6	756	2	A88679	protein H06H21.10
31	809.5	13.5	691	2	T41724	probable adenosine
32	583	9.7	424	2	T42662	hypothetical prote
33	440	7.4	918	2	F86709	cation-transportin
34	438.5	7.3	1160	2	T31688	Ca2+-transporting
35	427	7.1	1205	2	A35547	Ca2+-transporting
36	420.5	7.0	890	2	H69877	calcium-transporti
37	420	7.0	1203	2	S54357	plasma membrane Ca
38	417.5	7.0	1030	2	T00812	Ca2+-transporting
39	417	7.0	1198	2	B28065	cation-transportin
40	415.5	6.9	897	2	H86905	cation-transportin
41	414.5	6.9	902	2	C83964	cation-transportin
42	413	6.9	1169	2	S54356	Ca2+-transporting
43	401.5	6.7	1243	2	S22393	Ca2+-transporting
44	396.5	6.6	1159	2	A34308	Ca2+-transporting
45	394.5	6.6	1025	2	T45811	Ca2+-transporting

ALIGNMENTS

```
RESULT 1
T30869
probable adenosinetriphosphatase (EC 3.6.1.3) - mouse
N;Alternate names: chromaffin granule ATPase II; P-type ATPase
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30869
R;Pradhan, D.; Blackman, C.F.; Williamson, P.; Schlegel, R.A.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z20912
A;Accession: T30869
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1149 <PRA>
A;Cross-references: UNIPROT:P70704; UNIPARC:UPI00002773D; EMBL:U75321; NID:g1663647;
C;Keywords: hydrolase

Query Match            69.1%;   Score 4133;   DB 2;   Length 1149;
Best Local Similarity  68.3%;   Pred. No. 1.1e-280;
Matches  781;   Conservative 150;   Mismatches 191;   Indels 22;   Gaps  4;

Qy      1 MSRATSVGDQLEAPARTIYLNQPHLNKFRDNRISTAKYSVLTFLPRFLYEQIRRAANAPP 60
            :| |||||||||||  :  :||:|  :|      :  || :  : |||||||||||   |||||::
Db     24 VSEKTSLADQEB--VRTIFINQPQLTKFCNNHVSTAKYNVITFLPRFLYSQFRRAANSPF 81

Qy     61 LFIALLQQIPDVSPTGRYTTLVPLIIILTIAGIKEIVRDFKRHKADNAVNKKKTIVLRNG 120
            ||||||||||||||||||||||||| :  ::| ||| :|||||||||||||  ||||||
Db     82 LFIALLQQIPDVSPTGRYTTLVPLLFILAVAAIKEIIEDIKRHKADNAVNKKQTQVLRNG 141

Qy    121 MWHTIMWKEVAVGDIVKVNGQYLPADVVLLSSSEPQAMCYVETANLDGETNLKIRQGLS 180
            :  | :::|| ||||||   : :|||||||||||||||||:|||||||||:|||||||:
Db    142 AWEIVHWEKVNVGDIVIIKGKEYIPADFVLLSSEPPQAMCYIETSNLDGETNLKIRQGLP 201

Qy    181 HTADMQTREVLMKLSGTIECEGPNRHLYDFTGNLNLDGKSLVALGPDQILLRGTQLRNTQ 240
            :| :: |   :| :||  ||  |  || ||| ||| ||::|| |:|   || ||  |||||
Db    202 ATSDIKDIDSLMRISGRIECBSPNRHLYDFVGNIRLDGHGTVPLGADQIILRGAQLRNTQ 261

Qy    241 WVFGIVVYTGHDTKLMQNSTKAPLKRSNVEKVTNVQIILVLPGILLVMALVSSAGALYWNR 300
            |:|||||||||||||||||||:||||:| | | |:|||:|| :|::| |:||:||||||
Db    262 WVHGIVVYTGHDTKLMQNSTSPPLKLSNVERITNVQIILPCILIAMSLVCSVGSAIWNR 321

Qy    301 SHGEKNWYIKKMDTTSDNFGYNLLTPIILYNNLIPISLLVTLEVVKYTQALFINWDTDMY 360
            :| |::|| ||  :  :::| |:|  :|::| |||:||| |:::|| ||: ||::|| :  :
Db    322 RHSGKDWYLHLHYGGASNFGLNFLTFIILPLNNLLPISLLVTLLVVKFTQAYFINWDLDWH 381

Qy    361 YIGNDTPAMARTSNLNELGQVKYLFSDKTGTLTCNIMNFKKCSIAGVTYGHFPELAREP 420
            | ||| ||:||||||||||||||| ||||||||||||||||  |||  |:   | :| :|
Db    382 YEPTDTAAMARTSNLNELGQVKYIFSDKTGTLTCNVMQFKKCTIAGVAYG-------- 432

Qy    421 SSDDFCRMPPPCSDSCDPDPRLLRNIEDRHPTAPCIQEFLTLLAVCHTVVPEKDGDNII 480
             :  :: | |:  :  ||:: :||:||::|||  ||| |:|| |||:|||:||   |||
Db    433 -------GDBKTFNDPSLLDNLQNNHPTAPIICBFLTMWAVCHTAVPRREGDKII 485
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